IN THE SPECIFICATION

Please amend paragraph 74 of the specification as published (which begins on page 13 , line 27 of the application as filed) as follows:

The existing pattern discovery algorithm "TEIRESIAS" discovers patterns in multiple sequences that satisfy user-defined criteria such as minimum support, width etc. This algorithm is generally available and is, for example, available in the World Wide Web (www) at ~~cbcsrv.watson.ibm.com/tspd.html~~ cbcsrv(dot)Watson(dot)ibm(dot)com/tspd (dot)html. The TEIRESIAS algorithm is performed for these sequences and the Match-Set entries generated for Φα are shown in Table 1 above. The results are presented in Table 2 below, which is a table of Match-Set entries generated by the TEIRESIAS algorithm for the replets.

Please amend paragraph 81 of the specification as published (which begins on page 16 , line 16 of the application as filed) as follows:

Fig. 5 ~~4~~ presents a base-replet-sequence-matrix 500 ~~400~~ that is modified to accommodate the overlapping pattern {aa..a…a} and the schematic representation of the resulting replet-sequence-matrix. The base-replet-connector allows the resolving of the base pattern that was chosen against the non-base pattern (In this case, the pattern is {aaataa..aaa}).

Please amend paragraph 84 of the specification as published (which begins on page 16 , line 24 of the application as filed) as follows:

Fig. 6 ~~5~~ presents a replete-sequence-matrix 600 ~~500~~ that is modified to include a new replet {actata}. This new replet is a sub-string of the current replet {tactata…..ttac}. Thus base-replet connectors ARE added from actata's replet instances to the corresponding tactata…..ttac's replet instances.